

Computer-based methods are useful for screening a nucleic acid sequence for efficient translation in a predetermined host. These methods involve providing a 3'-end terminal ribosomal nucleic acid (rRNA) sequence, providing a substrate nucleic acid sequence, and detecting the presence or absence of a three-base binding strength (*i.e.*, binding energy) periodic cycle and/or phase between the ribosomal nucleic acid sequence and the substrate nucleic acid sequence through the substrate nucleic acid sequence. The presence of the three base periodic binding strength cycle and/or correct phase through the substrate nucleic acid sequence indicates that the substrate nucleic acid sequence is a candidate for efficient translation in the host.